



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/529,043B

DATE: 02/20/2002

TIME: 16:57:58

Input Set : A:\Fzj010-1.txt

Output Set: N:\CRF3\02202002\I529043B.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Forschungszentrum Juelich GmbH
 6 <120> TITLE OF INVENTION: Method for microbial production of amino acids of the
 7 aspartate and/or glutamate family and agents which can
 8 be used in said method
 10 <130> FILE REFERENCE: 1
 12 <140> CURRENT APPLICATION NUMBER: 09/529,043B
 13 <141> CURRENT FILING DATE: 2000-04-03
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP98/06210
 16 <151> PRIOR FILING DATE: 1998-09-30
 18 <160> NUMBER OF SEQ ID NOS: 4
 20 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3728
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Corynebacterium glutamicum
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (165)..(3587)
 30 <223> OTHER INFORMATION: pyruvate carboxylase
 32 <400> SEQUENCE: 1

E--> 33 cgcaaccgtg cttgaagtcg tgcaggtcag gggagtgttg cccgaaaaca ttgagaggaa
 34 60
 E--> 36 aacaaaaacc gatgtttgat tgggggaatc gggggttacg atactaggac gcagtgactg
 37 120
 E--> 39 ctatcaccct tggcggtctc ttgttgaaag gaataattac tcta gtg tcg act cac
 40 176
 41
 42 Val Ser Thr His
 1
 E--> 44 aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc
 45 224
 46 Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg
 47 5 10 15 20
 E--> 49 ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca
 50 272
 51 Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala
 52 25 30 35
 E--> 54 gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc
 55 320
 56 Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg

60 format
 error
 120
 ↓

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```

57          40          45          50
E--> 59 tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc
60 368
61 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val
62          55          60          65
E--> 64 aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt
65 416
66 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val
67          70          75          80
E--> 69 aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc
70 464
71 Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala
72 85          90          95          100
E--> 74 cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca
75 512
76 Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro
77          105          110          115
E--> 79 acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc
80 560
81 Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr
82          120          125          130
E--> 84 gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc
85 608
86 Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser
87          135          140          145
E--> 89 aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc
90 656
91 Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro
92          150          155          160
E--> 94 atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt
95 704
96 Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe
97 165          170          175          180
E--> 99 gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt
100 752
101 Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg
102          185          190          195
E--> 104 gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct
105 800
106 Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala
107          200          205          210
E--> 109 gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act
110 848
111 Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr
112          215          220          225
E--> 114 gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt
115 896
116 Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg
117          230          235          240

```

*same
error*

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```

E--> 119 cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa
      120 944
      121 His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu
      122 245                250                255                260
E--> 124 ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att
      125 992
      126 Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile
      127                265                270                275
E--> 129 ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc
      130 1040
      131 Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly
      132                280                285                290
E--> 134 aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc
      135 1088
      136 Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr
      137                295                300                305
E--> 139 gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc
      140 1136
      141 Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg
      142                310                315                320
E--> 144 ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag
      145 1184
      146 Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys
      147 325                330                335                340
E--> 149 atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat
      150 1232
      151 Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp
      152                345                350                355
E--> 154 cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc
      155 1280
      156 Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg
      157                360                365                370
E--> 159 tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt
      160 1328
      161 Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly
      162                375                380                385
E--> 164 ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc
      165 1376
      166 Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys
      167                390                395                400
E--> 169 cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg
      170 1424
      171 Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu
      172 405                410                415                420
E--> 174 gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt
      175 1472
      176 Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg
      177                425                430                435
E--> 179 gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga

```

same

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```

180 1520
181 Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly
182          440          445          450
E--> 184 ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat
185 1568
186 Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp
187          455          460          465
E--> 189 gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag
190 1616
191 Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys
192          470          475          480
E--> 194 cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg
195 1664
196 Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu
197 485          490          495          500
E--> 199 cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc ctg
200 1712
201 Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg Leu
202          505          510          515
E--> 204 aag cag ctt ggc cca gcc gcg ttt gct cgt gat ctc cgt gag cag gac
205 1760
206 Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu Arg Glu Gln Asp
207          520          525          530
E--> 209 gca ctg gca gtt act gat acc acc ttc cgc gat gca cac cag tct ttg
210 1808
211 Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu
212          535          540          545
E--> 214 ctt gcg acc cga gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc
215 1856
216 Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala
217          550          555          560
E--> 219 gtc gca aag ctg act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc
220 1904
221 Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly
222 565          570          575          580
E--> 224 gcg acc tac gat gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac
225 1952
226 Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp
227          585          590          595
E--> 229 agg ctc gac gag ctg cgc gag gcg atg ccg aat gta aac att cag atg
230 2000
231 Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met
232          600          605          610
E--> 234 ctg ctt cgc ggc cgc aac acc gtg gga tac acc ccg tac cca gac tcc
235 2048
236 Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser
237          615          620          625
E--> 239 gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc
240 2096

```

same

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```

241 Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile
242      630      635      640
E--> 244 ttc cgc atc ttc gac gcg ctt aac gac gtc tcc cag atg cgt cca gca
245 2144
246 Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala
247 645      650      655      660
E--> 249 atc gac gca gtc ctg gag acc aac acc gcg gta gcc gag gtg gct atg
250 2192
251 Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met
252      665      670      675
E--> 254 gct tat tct ggt gat ctc tct gat cca aat gaa aag ctc tac acc ctg
255 2240
256 Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu
257      680      685      690
E--> 259 gat tac tac cta aag atg gca gag gag atc gtc aag tct ggc gct cac
260 2288
261 Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His
262      695      700      705
E--> 264 atc ttg gcc att aag gat atg gct ggt ctg ctt cgc cca gct gcg gta
265 2336
266 Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val
267      710      715      720
E--> 269 acc aag ctg gtc acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac
270 2384
271 Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His
272 725      730      735      740
E--> 274 gtg cac acc cac gac act gcg ggt ggc cag ctg gca acc tac ttt gct
275 2432
276 Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala
277      745      750      755
E--> 279 gca gct caa gct ggt gca gat gct gtt gac ggt gct tcc gca cca ctg
280 2480
281 Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu
282      760      765      770
E--> 284 tct ggc acc acc tcc cag cca tcc ctg tct gcc att gtt gct gca ttc
285 2528
286 Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe
287      775      780      785
E--> 289 gcg cac acc cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac
290 2576
291 Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp
292      790      795      800
E--> 294 ctc gag ccg tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag
295 2624
296 Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu
297 805      810      815      820
E--> 299 tct gga acc cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca
300 2672
301 Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro

```

same

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```

      302              825              830              835
E--> 304 ggc gga cag ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt
      305 2720
      306 Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu
      307              840              845              850
E--> 309 gcg gat cgt ttc gaa ctc atc gaa gac aac tac gca gcc gtt aat gag
      310 2768
      311 Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ala Val Asn Glu
      312              855              860              865
E--> 314 atg ctg gga cgc cca acc aag gtc acc cca tcc tcc aag gtt gtt ggc
      315 2816
      316 Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly
      317              870              875              880
E--> 319 gac ctc gca ctc cac ctc gtt ggt gcg ggt gtg gat cca gca gac ttt
      320 2864
      321 Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
      322 885              890              895              900
E--> 324 gct gcc gat cca caa aag tac gac atc cca gac tct gtc atc gcg ttc
      325 2912
      326 Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
      327              905              910              915
E--> 329 ctg cgc ggc gag ctt ggt aac cct cca ggt ggc tgg cca gag cca ctg
      330 2960
      331 Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
      332              920              925              930
E--> 334 cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc aag gca cct ctg acg
      335 3008
      336 Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
      337              935              940              945
E--> 339 gaa gtt cct gag gaa gag cag gcg cac ctc gac gct gat gat tcc aag
      340 3056
      341 Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
      342              950              955              960
E--> 344 gaa cgt cgc aat agc ctc aac cgc ctg ctg ttc ccg aag cca acc gaa
      345 3104
      346 Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
      347 965              970              975              980
E--> 349 gag ttc ctc gag cac cgt cgc cgc ttc ggc aac acc tct gcg ctg gat
      350 3152
      351 Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
      352              985              990              995
E--> 354 gat cgt gaa ttc ttc tac ggc ctg gtc gaa ggc cgc gag act ttg atc
      355 3200
      356 Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
      357              1000              1005              1010
E--> 359 cgc ctg cca gat gtg cgc acc cca ctg ctt gtt cgc ctg gat gcg atc
      360 3248
      361 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
      362              1015              1020              1025

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same

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```

E--> 364 tct gag cca gac gat aag ggt atg cgc aat gtt gtg gcc aac gtc aac
      365 3296
      366 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
      367 1030 1035 1040
E--> 369 ggc cag atc cgc cca atg cgt gtg cgt gac cgc tcc gtt gag tct gtc
      370 3344
      371 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
      372 1045 1050 1055 1060
E--> 374 acc gca acc gca gaa aag gca gat tcc tcc aac aag ggc cat gtt gct
      375 3392
      376 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
      377 1065 1070 1075
E--> 379 gca cca ttc gct ggt gtt gtc acc gtg act gtt gct gaa ggt gat gag
      380 3440
      381 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
      382 1080 1085 1090
E--> 384 gtc aag gct gga gat gca gtc gca atc atc gag gct atg aag atg gaa
      385 3488
      386 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
      387 1095 1100 1105
E--> 389 gca aca atc act gct tct gtt gac ggc aaa atc gat cgc gtt gtg gtt
      390 3536
      391 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val
      392 1110 1115 1120
E--> 394 cct gct gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc
      395 3584
      396 Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
      397 1125 1130 1135 1140
E--> 399 taa acctttctgt aaaaagcccc gcgtcttct catggaggag gcggggcttt
      400 3637
E--> 403 ttggggccaag atgggagatg ggtgagttgg atttggtctg attcgacact ttaagggca
      404 3697
E--> 406 gagatttgaa gatggagacc aaggctcaaa g
      407 3728
      563 <210> SEQ ID NO: 3
      564 <211> LENGTH: 19
      565 <212> TYPE: DNA
      566 <213> ORGANISM: Artificial Sequence
      568 <220> FEATURE:
      569 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer
      571 <400> SEQUENCE: 3
E--> 572 cgtcttcacg gaaatgaac
      573 19
      576 <210> SEQ ID NO: 4
      577 <211> LENGTH: 19
      578 <212> TYPE: DNA
      579 <213> ORGANISM: Artificial Sequence
      581 <220> FEATURE:
      582 <223> OTHER INFORMATION: Description of Artificial Sequence: PCR primer

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*same**same*

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584 <400> SEQUENCE: 4

E--> 585 acggtggtga tccggcact

586 19

same

VERIFICATION SUMMARY

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Input Set : A:\Fzj010~1.txt

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L:33 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:572 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:3
L:585 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:19 SEQ:4